



131

SEQUENCE LISTING

<110> NICKlin, Martin
Barton, Jenny

<120> IL-1L1 GENE AND POLYPEPTIDE PRODUCTS

<130> MSA-021.01

<140> 09/617,720

<141> 2000-07-17

<160> 54

<170> PatentIn Ver. 2.1

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Ala Gly Lys Val Ile Lys Gly Glu Glu Ile Ser Val Val Pro Asn Arg
35 40 45

Trp Leu Asp Ala Ser Leu Ser Pro Val Ile Leu Gly Val Gln Gly Gly
50 55 60

Ser Gln Cys Leu Ser Cys Gly Val Gly Gln Glu Pro Thr Leu Thr Leu
65 70 75 80

Glu Pro Val Asn Ile Met Glu Leu Tyr Leu Gly Ala Lys Glu Ser Lys
85 90 95

Ser Phe Thr Phe Tyr Arg Arg Asp Met Gly Leu Thr Ser Ser Phe Glu
100 105 110

Ser Ala Ala Tyr Pro Gly Trp Phe Leu Cys Thr Val Pro Glu Ala Asp
115 120 125

Gln Pro Val Arg Leu Thr Gln Leu Pro Glu Asn Gly Gly Trp Asn Ala
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Pro Ile Thr Asp Phe Tyr Phe Gln Gln Cys Asp
145 150 155

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<213> Murine sp.

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Lys Val Leu Tyr Leu His Asn Asn Gln Leu Leu Ala Gly Gly Leu His
20 25 30

Ala Glu Lys Val Ile Lys Gly Glu Glu Ile Ser Val Val Pro Asn Arg
35 40 45

Ala Leu Asp Ala Ser Leu Ser Pro Val Ile Leu Gly Val Gln Gly Gly
50 55 60

Ser Gln Cys Leu Ser Cys Gly Thr Glu Lys Gly Pro Ile Leu Lys Leu
65 70 75 80

134

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Glu Pro Val Asn Ile Met Glu Leu Tyr Leu Gly Ala Lys Glu Ser Lys
85 90 95

Ser Phe Thr Phe Tyr Arg Arg Asp Met Gly Leu Thr Ser Ser Phe Glu
100 105 110

Ser Ala Ala Tyr Pro Gly Trp Phe Leu Cys Thr Ser Pro Glu Ala Asp
115 120 125

Gln Pro Val Arg Leu Thr Gln Ile Pro Glu Asp Pro Ala Trp Asp Ala
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<212> PRT

<213> Artificial Sequence

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polypeptide sequence

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20 25 30

Ala Lys Val Ile Lys Gly Glu Glu Ile Ser Val Val Pro Asn Arg Leu
35 40 45

Asp Ala Ser Leu Ser Pro Val Ile Leu Gly Val Gln Gly Ser Gln
50 55 60

Cys Leu Ser Cys Gly Pro Leu Leu Glu Pro Val Asn Ile Met Glu Leu
65 70 75 80

Tyr Leu Gly Ala Lys Glu Ser Lys Ser Phe Thr Phe Tyr Arg Arg Asp
85 90 95

Met Gly Leu Thr Ser Ser Phe Glu Ser Ala Ala Tyr Pro Gly Trp Phe
100 105 110

Leu Cys Thr Pro Glu Ala Asp Gln Pro Val Arg Leu Thr Gln Pro Glu
115 120 125

Trp Ala Pro Ile Thr Asp Phe Tyr Phe Gln Gln Cys Asp
130 135 140

<210> 8

<211> 138

<212> PRT

<213> Homo sapiens

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<400> 8
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20 25 30

Lys Ile Asp Val Val Pro Ile Glu Pro His Ala Leu Phe Leu Gly Ile
35 40 45

His Gly Gly Lys Met Cys Leu Ser Cys Val Lys Ser Gly Asp Glu Thr
50 55 60

Arg Leu Gln Leu Glu Ala Val Asn Ile Thr Asp Leu Ser Glu Asn Arg
65 70 75 80

Lys Gln Asp Lys Arg Phe Ala Phe Ile Arg Ser Asp Ser Gly Pro Thr
85 90 95

Thr Ser Phe Glu Ser Ala Ala Cys Pro Gly Trp Phe Leu Cys Thr Ala
100 105 110

Met Glu Ala Asp Gln Pro Val Ser Leu Thr Asn Met Pro Asp Glu Gly
115 120 125

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Consensus
polypeptide sequence

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20 25 30

Glu Val Asn Ile Leu Lys Lys Phe Phe Arg Asp Gly Thr Ser Phe Glu
35 40 45

Ser Ala Ala Pro Gly Trp Phe Leu Cys Thr Glu Ala Asp Gln Pro Val
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Leu Thr Pro Gly Thr Phe Tyr Phe Gln
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<212> DNA
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<210> 12
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Conserved
consensus DNA sequence

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<210> 13
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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Recombinant
IBR polypeptide

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Lys Val Leu Tyr Leu His Asn Asn Gln Leu Leu Ala Gly Gly Leu His
20 25 30

Ala Gly Lys Val Ile Lys Gly Glu Glu Ile Ser Val Val Pro Asn Arg
35 40 45

Trp Leu Asp Ala Ser Leu Ser Pro Val Ile Leu Gly Val Gln Gly Gly
50 55 60

Ser Gln Cys Leu Ser Cys Gly Val Gly Gln Glu Pro Thr Leu Thr Leu
65 70 75 80

Glu Pro Val Asn Ile Met Glu Leu Tyr Leu Gly Ala Lys Glu Ser Lys
85 90 95

Ser Phe Thr Phe Tyr Arg Arg Asp Met Gly Leu Thr Ser Ser Phe Glu
100 105 110

Ser Ala Ala Tyr Pro Gly Trp Phe Leu Cys Thr Val Pro Glu Ala Asp
115 120 125

Gln Pro Val Arg Leu Thr Gln Leu Pro Glu Asn Gly Gly Trp Asn Ala
130 135 140

Pro Ile Thr Asp Phe Tyr Phe Gln Gln Cys Asp
145 150 155

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<223> Description of Artificial Sequence: Recombinant
IBR polypeptide

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Val Leu Tyr Leu His Asn Asn Gln Leu Leu Ala Gly Gly Leu His Ala
20 25 30

Gly Lys Val Ile Lys Gly Glu Glu Ile Ser Val Val Pro Asn Arg Trp
35 40 45

Leu Asp Ala Ser Leu Ser Pro Val Ile Leu Gly Val Gln Gly Gly Ser
50 55 60

Gln Cys Leu Ser Cys Gly Val Gly Gln Glu Pro Thr Leu Thr Leu Glu
65 70 75 80

138
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Pro Val Asn Ile Met Glu Leu Tyr Leu Gly Ala Lys Glu Ser Lys Ser
85 90 95

Phe Thr Phe Tyr Arg Arg Asp Met Gly Leu Thr Ser Ser Phe Glu Ser
100 105 110

Ala Ala Tyr Pro Gly Trp Phe Leu Cys Thr Val Pro Glu Ala Asp Gln
115 120 125

Pro Val Arg Leu Thr Gln Leu Pro Glu Asn Gly Gly Trp Asn Ala Pro
130 135 140

Ile Thr Asp Phe Tyr Phe Gln Gln Cys Asp
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<210> 15

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<212> PRT

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<223> Description of Artificial Sequence: Recombinant
IBR polypeptide

<400> 15

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Ala Leu Lys Val Leu Tyr Leu His Asn Asn Gln Leu Leu Ala Gly Gly
20 25 30

Leu His Ala Gly Lys Val Ile Lys Gly Glu Glu Ile Ser Val Val Pro
35 40 45

Asn Arg Trp Leu Asp Ala Ser Leu Ser Pro Val Ile Leu Gly Val Gln
50 55 60

Gly Gly Ser Gln Cys Leu Ser Cys Gly Val Gly Gln Glu Pro Thr Leu
65 70 75 80

Thr Leu Glu Pro Val Asn Ile Met Glu Leu Tyr Leu Gly Ala Lys Glu
85 90 95

Ser Lys Ser Phe Thr Phe Tyr Arg Arg Asp Met Gly Leu Thr Ser Ser
100 105 110

Phe Glu Ser Ala Ala Tyr Pro Gly Trp Phe Leu Cys Thr Val Pro Glu
115 120 125

Ala Asp Gln Pro Val Arg Leu Thr Gln Leu Pro Glu Asn Gly Gly Trp
130 135 140

Asn Ala Pro Ile Thr Asp Phe Tyr Phe Gln Gln Cys Asp
145 150 155

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<213> Homo sapiens

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<210> 17
<211> 16
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<400> 17
Met Ala Gly Arg Lys Asp Arg Gly Arg Lys Glu Gly Glu Gly Lys Glu
1 5 10 15

<210> 18
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<210> 20
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<210> 21
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<400> 21
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<212> DNA
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<210> 23
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Ala Gly Lys Val Ile Lys Gly Glu Glu Ile Ser Val Val Pro Asn Arg
35 40 45

Trp Leu Asp Ala Ser Leu Ser Pro Val Ile Leu Gly Val Gln Gly Gly
50 55 60

Ser Gln Cys Leu Ser Cys Gly Val Gly Gln Glu Pro Thr Leu Thr Leu
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Glu Val Asn Ile Met Glu Leu Tyr Leu Gly Ala Lys Glu Ser Lys Ser
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Phe Thr Phe Tyr Arg Arg Asp Met
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<210> 42
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<212> PRT
<213> Homo sapiens

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20 25 30

Gly Pro Asn Val Asn Leu Glu Glu Lys Ile Asp Val Val Pro Ile Glu
35 40 45

Pro His Ala Leu Phe Leu Gly Ile His Gly Gly Lys Met Cys Leu Ser
50 55 60

Cys Val Lys Ser Gly Asp Glu Thr Arg Leu Gln Leu Glu Val Asn Ile
65 70 75 80

Thr Asp Leu Ser Glu Asn Arg Lys Gln Asp Lys Arg Phe Ala Phe Ile
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Arg Ser Asp Ser
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<212> DNA
<213> Homo sapiens

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145
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<210> 44
<211> 152
<212> PRT
<213> *Homo sapiens*

146
16

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Arg Pro Ser Gly Arg Lys Ser Ser Lys Met Gln Ala Phe Arg Ile Trp
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Asp Val Asn Gln Lys Thr Phe Tyr Leu Arg Asn Asn Gln Leu Val Ala
20 25 30

Gly Tyr Leu Gln Gly Pro Asn Val Asn Leu Glu Glu Lys Ile Asp Val
35 40 45

Val Pro Ile Glu Pro His Ala Leu Phe Leu Gly Ile His Gly Gly Lys
50 55 60

Met Cys Leu Ser Cys Val Lys Ser Gly Asp Glu Thr Arg Leu Gln Leu
65 70 75 80

Glu Ala Val Asn Ile Thr Asp Leu Ser Glu Asn Arg Lys Gln Asp Lys
85 90 95

Arg Phe Ala Phe Ile Arg Ser Asp Ser Gly Pro Thr Thr Ser Phe Glu
100 105 110

Ser Ala Ala Cys Pro Gly Trp Phe Leu Cys Thr Ala Met Glu Ala Asp
115 120 125

Gln Pro Val Ser Leu Thr Asn Met Pro Asp Glu Gly Val Met Val Thr
130 135 140

Lys Phe Tyr Phe Gln Glu Asp Glu
145 150

<210> 45
<211> 153
<212> PRT
<213> Homo sapiens

<400> 45
Ala Pro Val Arg Ser Leu Asn Cys Thr Leu Arg Asp Ser Gln Gln Lys
1 5 10 15

Ser Leu Val Met Ser Gly Pro Tyr Glu Leu Lys Ala Leu His Leu Gln
20 25 30

Gly Gln Asp Met Glu Gln Gln Val Val Phe Ser Met Ser Phe Val Gln
35 40 45

Gly Glu Glu Ser Asn Asp Lys Ile Pro Val Ala Leu Gly Leu Lys Glu
50 55 60

Lys Asn Leu Tyr Leu Ser Cys Val Leu Lys Asp Asp Lys Pro Thr Leu
65 70 75 80

Gln Leu Glu Ser Val Asp Pro Lys Asn Tyr Pro Lys Lys Met Glu
85 90 95

Lys Arg Phe Val Phe Asn Lys Ile Glu Ile Asn Asn Lys Leu Glu Phe
100 105 110

147

Glu Ser Ala Gln Phe Pro Asn Trp Tyr Ile Ser Thr Ser Gln Ala Glu
115 120 125

Asn Met Pro Val Phe Leu Gly Gly Thr Lys Gly Gly Gln Asp Ile Thr
130 135 140

Asp Phe Thr Met Gln Phe Val Ser Ser
145 150

<210> 46
<211> 159
<212> PRT
<213> Homo sapiens

<400> 46
Ser Ala Pro Phe Ser Phe Leu Ser Asn Val Lys Tyr Asn Phe Met Arg
1 5 10 15

Ile Ile Lys Tyr Glu Phe Ile Leu Asn Asp Ala Leu Asn Gln Ser Ile
20 25 30

Ile Arg Ala Asn Asp Gln Tyr Leu Thr Ala Ala Leu His Asn Leu
35 40 45

Asp Glu Ala Val Lys Phe Asp Met Gly Ala Tyr Lys Ser Ser Lys Asp
50 55 60

Asp Ala Lys Ile Thr Val Ile Leu Arg Ile Ser Lys Thr Gln Leu Tyr
65 70 75 80

Val Thr Ala Gln Asp Glu Asp Gln Pro Val Leu Leu Lys Glu Met Pro
85 90 95

Glu Ile Pro Lys Thr Ile Thr Gly Ser Glu Thr Asn Leu Leu Phe Phe
100 105 110

Trp Glu Thr His Gly Thr Lys Asn Tyr Phe Thr Ser Val Ala His Pro
115 120 125

Asn Leu Phe Ile Ala Thr Lys Gln Asp Tyr Trp Val Cys Leu Ala Gly
130 135 140

Gly Pro Pro Ser Ile Thr Asp Phe Gln Ile Leu Glu Asn Gln Ala
145 150 155

<210> 47
<211> 157
<212> PRT
<213> Homo sapiens

<400> 47
Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile Arg Asn Leu Asn
1 5 10 15

148
18

Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro Leu Phe Glu Asp
20 25 30

Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg Thr Ile Phe Ile
35 40 45

Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met Ala Val Thr Ile
50 55 60

Ser Val Lys Cys Glu Lys Ile Ser Thr Leu Ser Cys Glu Asn Lys Ile
65 70 75 80

Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile Lys Asp Thr Lys
85 90 95

Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asn Lys
100 105 110

Met Gln Phe Glu Ser Ser Tyr Glu Gly Tyr Phe Leu Ala Cys Glu
115 120 125

Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys Glu Asp Glu Leu
130 135 140

Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu Asp
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<210> 48

<211> 6

<212> PRT

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<223> Description of Artificial Sequence: Consensus
peptide sequence

<220>

<221> MOD_RES

<222> (1)..(6)

<223> Xaa represents a variable amino acid

<400> 48

Leu Lys Xaa Leu Xaa Leu

1 5

<210> 49

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus
peptide sequence

<220>

<221> MOD_RES

149
x9

<222> (1)..(7)
<223> Xaa represents a variable amino acid

<400> 49
Ile Thr Asp Phe Xaa Xaa Gln
1 5

<210> 50
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus
peptide sequence

<220>
<221> MOD_RES
<222> (1)..(12)
<223> Xaa represents a variable amino acid

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Tyr Leu Xaa Asn Asn Gln Leu Xaa Ala Gly Xaa Leu
1 5 10

<210> 51
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus
peptide sequence

<220>
<221> MOD_RES
<222> (1)..(9)
<223> Xaa represents a variable amino acid

<400> 51
Leu Glu Xaa Val Asn Ile Xaa Xaa Leu
1 5

<210> 52
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus
peptide sequence

<220>
<221> MOD_RES
<222> (1)..(24)

150
20

a
<223> Xaa represents a variable amino acid

<400> 52

Thr Xaa Ser Phe Glu Ser Ala Ala Xaa Pro Gly Trp Phe Leu Cys Thr
1 5 10 15

Xaa Xaa Glu Ala Asp Gln Pro Val
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<210> 53

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Binding domain

<400> 53

Phe Gly Phe Arg
1

but
<210> 54

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: N-terminal
extension

<400> 54

Gly Ser Ser Gly Leu Arg Arg Ala Ser Leu Gly Ser Ser
1 5 10